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To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Date: \_\_\_\_\_

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known.

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Searcher: <u>Beverly C 4994</u>		NA Sequence (#)	<input type="checkbox"/> STN <input type="checkbox"/> Dialog
Searcher Phone #:		AA Sequence (#)	<input type="checkbox"/> Questel/Orbit <input type="checkbox"/> Dr. Link
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CC modulating the production of a T-helper type 2 associated cytokine.  
 CC Especially the method is useful in the inhibition of Th2 in allergy,  
 CC cancer or infections, and promotion of Th2 in autoimmune disease and  
 CC transplantation  
 Sequence 412 AA:

Query Match 100.0%; Score 2858; DB 28; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 2.68e-219; 0; Mismatches 0; Indels 0;  
 Matches 412; Conservative 0; Gaps 0;

Db 1 maepirgrgprsrgrgrrarrargrgeprarqparlpidvldvdivsdseevleval 60  
 Qy 1 MAEPLRGGRGPRSGGGRARRANGARGCPRARQSPARLIPDVLVDVSDSEEVLEVAD 60

Db 61 pvevpvarlpakpepdssdssegaagsgapaprtivrrrrlidgeapavpyysk 120  
 Qy 121 VQSSNLIPDNSSLLKLCSEPEDEADLINSSSPSEDDALPGSPWKRKKCEEEK 120

Db 181 kmeeppadispipqpsrnkskhtelqkirevnklqlrlsc1lpkqngspalqstd 240  
 Qy 181 KMEEPPDODISPLQPSSRNKSRRTEALKQLREVNLQDLDRSCLSPKQHGSPLAQSTD 240

Db 241 dervlveaqplpassrltikirkadirlvlpymsepqlqnvwdmahnlgsprnill 300  
 Qy 241 DERTLVBCPVQDQSSRLTILKIRKADIRLVLVLPYMRMSEBLQNYDHDMANHLGSPNRLILL 300

Db 301 fresselpatptsklikqvadidcvvlasseatetsqelirrvqekhmlleislp 360  
 Qy 301 FGSELSPLSTATPSLKLQVADIDCVVLAASSPATEISOELRLRVOKEKHOMLEISLP 360

Db 361 daplkvimshyeamglsghkisffffgtkkgeladgliesgliewg 412  
 Qy 361 DSPKVLMSHYEAMGLSGHKLSFFDCTKLSGKELPLDGLGESGDLLIEWG 412

RESULT 2  
 ID W50079 standard; Protein; 101 AA.  
 AC W50079;  
 DT 11-SEP-1998 (first entry)  
 DE Homo sapiens sentrin-1 polypeptide.  
 KW sentrin-1; protection; tumour necrosis factor; tnf; apoptosis;  
 FAS/APO-induced; tumour cell death; induction; tumour aggressiveness;  
 detection; determination.  
 OS Homo sapiens.  
 PN W09820038-A1.  
 PD 14-MAY-1998.  
 PP 05-NOV-1997; U20344.  
 PR 03-NOV-1996; US-030302.  
 PA (TEXA.) UNIV TEXAS SYSTEM.  
 PI Yen, ERI, DR  
 WPI: 98-2286868/25.  
 DR N-PSDB; V34364.

PT New isolated sentrin polypeptide(s) - which inhibit TNF receptor or  
 PT Fas/APO-induced apoptosis, used to develop products for inducing  
 PT cell death in tumours  
 PS Claim 4, Page 78, 120pp; English.  
 The sequence is that of the sentrin-1 polypeptide.

CC Sentrin polypeptides have the ability to protect or guard  
 CC cells from tumour necrosis factor (TNF) or Fas/APO induced  
 CC cell death (apoptosis). Inhibitors of the sentrin polypeptides,  
 CC e.g. antibodies, can be used for inducing cell death,  
 particularly in tumours. The products can also be used for  
 determining the aggressiveness of a tumour and for detection and  
 isolation of products. The sentrin polypeptide can also be used to  
 detect a ubiquitin conjugating enzyme polypeptide or PML polypeptide.  
 Sequence 101 AA;

Query Match 5.3%; Score 151; DB 32; Length 101;  
 Best Local Similarity 27.4%; Pred. No. 3.49e-02;

	Matches	Conservative	Mismatches	Indels	Gaps
Db	8	pstedlqdkkqgeyikivqkqddsei-hfvvmkmtthikkkesyvqrqgpmairflf	66		3
Qy	329	ASSEATETSQ-E-LRIVQSGEKHOMLEISLSPDPLKVMISHYEAAMGJSGHKLSFFF	386		3
Db	67	sqgriaadnhtpkelgmeediev	90		
Qy	387	DSTKLKGKELPADLGLESGLIEV	410		
RESULT	3				
ID	W07497	standard; Protein; 126 AA.			
AC	W07497;				
DT	18-FEB-1999	(first entry)			
DE	Human SMT3-like protein (HSMT3).				
KW	HSMTH; SMT3-like protein; recombinant; foetal development; inflammation; cancer; radiation; DNA repair; carcinogenic; ataxia telangiectasia; sunscreen; therapeutic; cell proliferative disease; antagonist; asthma; Crohn's disease; rheumatoid arthritis; ribozyme; chromosome mapping; immunosassay; drug; screening.				
OS	Homo sapiens.				
FH					
Key					
FT	Modified_site	12	/note= "potential phosphorylation site"		
FT	Modified_site	23	/note= "potential myristylation site"		
FT	Modified_site	34	/note= "potential phosphorylation site"		
FT	Modified_site	53	/note= "potential phosphoylation site"		
FT	Modified_site	63	/note= "potential myristylation site"		
FT	Modified_site	67	/note= "potential Nglycosylation site"		
FT	Modified_site	88	/note= "potential phosphorylation site"		
FT	Misc_difference	108	/note= "potential phosphorylation site" /label= "unknown" /note= "encoded by ANA"		
FT	PN	W09850545-A1.			
PD	12-NOV-1998.				
PP	05-MAY-1998; U08420.				
PR	09-MAY-1997; US-853974.				
PA	(INCY-) INCYTE PHARM INC.				
PI	Hiliman, JL, Shah, P;				
DR	WPI: 98-034720/03.				
DR	N-PSDB; V73504.				
PT	New human SMT3-like protein - for treatment, prevention and diagnosis of cancer and inflammation, and for promoting DNA repair				
PT	Claim 1; Fig 1A-B; 55pp; English.				
PS	This represents a human SMT3-like protein (HSMT3). Host cells transformed with expression vectors containing the HSMT3 nucleic acid are used for the recombinant production of the protein. HSMT3, expressed in COKA cell lines associated with foetal development, inflammation, cancer and radiation damage, is used to promote DNA repair (before, during or after exposure to damage from radiation or carcinogenic compounds). The polypeptide can be used to treat patients with ataxia telangiectasia, or related diseases, who are undergoing radiation treatment for cancers associated with these diseases, or it is added to sunscreens. The HSMT3 protein is also used for the generation of antibodies and screening for specific binding agents (potential therapeutics). Antagonists are used to treat or prevent cell proliferative diseases, especially cancer and inflammation (e.g. asthma, Crohn's disease, rheumatoid arthritis). The HSMT3 nucleic acid and its fragments are used as antisense/ribozyme therapeutics; for detecting and quantifying gene expression; for isolating related sequences and for chromosome mapping. The antibodies are used directly therapeutic antagonists; for delivering drugs to cells expressing HSMT3; as immunoassay reagents for diagnosis or monitoring disease or treatment; in competitive drug screens and to isolate the protein from natural sources.				
SQ	Sequence 126 AA;				



are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V59511 for described uses).

Sequence	IUPAC AA;
Query Match	5.2%
Best Local Similarity	28.6%
Matches	20; Conservative
Score	149; DB 37; Length 102;
Prec.	No. 4.74e-07
Mismatches	26; Indels 1; Gaps 1;
22	iklvqigdsei-hfkvkmthlikkikesyqrqavpmnslrfifegqriadnhtpkel 80
341	LRLRVQGKEKKHOMLEISLSPDSPLKVLMHSYTEAMGLSGHKLSPFDGTLKSGKELPADL 400
81	gmeedqviev 90
401	GIESGDLIEV 410

CC	cyclase.
PI	Sequence 1184 AA;
DR	WPI; 98-336114/30.
DR	Non-M, non-O HIV-1 strain YBF30 - useful for diagnosis and
PT	Best Local Similarity 50.0%; Pred. No. 1.7e+01; Length 1184;
PT	Mismatches 9; Indels 8; Gaps 2;
PS	Matches 19; Conservative 9; Mismatches 8; Indels 2; Gaps 2;
CC	This sequence represents the rev protein from the non-M (major), non-O
CC	(Outlier) HIV-1 strain YBF30 (CNCM I-1753), isolated from the Cameroon.
CC	The HIV strain YBF30 (see V60751 for complete genome), peptides, antibodies and
CC	oligonucleotides derived from it (see V60752-V60798 and W68473-W68482) are used for diagnosis or immunisation against non-M, non-O HIV-1
CC	infections. The oligonucleotides, peptides and antibodies can also be
CC	used for typing HIV strains.
SQ	Sequence 1184 AA;
AC	R32882;
AC	17-JUN-1993 (first entry)
DE	Cardiac adenylyl cyclase type V.
KW	CACV; therapy; diagnostic; cardiac function; cyclic AMP; cAMP; heart failure.
OS	Canis familiaris.
DR	EP-5-29622-A.
PR	03-MAR-1993.
PR	27-AUG-1992; 114537.
PA	29-AUG-1991; US-751460.
PA	(AMCY ) AMERICAN CYANAMID CO.
PI	Ishikawa Y, Kohki AF;
DR	WRI; 93-068888/09.
PT	N-PSDB; Q37543;
PT	Isolated nucleic acid mol. encoding Cardiac adenylyl cyclase type
PT	V - useful for determining and modifying cardiac function
PS	Claim 4; Page 15-27; 38pp; English.
CC	Left ventricular tissue of canine heart was used as a source of mRNA.
CC	A cDNA library was prep'd. in lambda gt10 phage. A 970 bp Aat-HincII fragment from type I adeyyl cyclase cDNA was used as prob. The clones isolated were used to obtain cDNA encoding CACV. This probe may also be used to screen a human cardiac cDNA library to obtain the cDNA encoding human CACV. CACV, its analogues and antibodies are useful in therapy or diagnostic assays, e.g. in modifying and determining cardiac function. A decrease in CACV content of the heart contributes to impaired cAMP prodn. and in heart failure. The CACV can also be used to screen for cpds. which stimulate or inhibit the activity of the cyclase.
SQ	Sequence 1184 AA;
RESULT	9
ID	wf8479 standard; Protein; 122 AA.
AC	WF8479;
AC	01-DEC-1998 (first entry)
DE	HIV-1 strain YBF30 rev protein.
KW	HIV-1 strain YBF30; antibody; oligonucleotide; diagnosis; immunisation; infection; typing; rev.
OS	Human immunodeficiency virus type 1.
FH	key location/qualifiers
FT	Misc_difference 104
FT	/label= unknown /note= "encoded by TGA"
FT	12-JUN-1998.
PR	09-DEC-1996; 015087.
PR	09-DEC-1996; FR-015087.
PA	(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA	(INRM ) INSTITUT NATIONAL SANTE & RECH MEDICALE.
PA	(INSP ) INST PASTEUR.
PA	Baile-Sinoussi F, Loussert-Ajaka I, Maclere P, Saragosti S,
RESULT	9
ID	wf8479 standard; Protein; 122 AA.
AC	WF8479;
AC	01-DEC-1998 (first entry)
DE	HIV-1 strain YBF30 rev protein.
KW	HIV-1 strain YBF30; antibody; oligonucleotide; diagnosis; immunisation; infection; typing; rev.
OS	Human immunodeficiency virus type 1.
FH	key location/qualifiers
FT	Misc_difference 104
FT	/label= unknown /note= "encoded by TGA"
FT	13-JUN-1996.
PE	08-DEC-1995; U16216.
PR	08-DEC-1994; US-355700.
PA	(FOXC-) FOX CHASE CANCER CENT.
PA	(UYME-) UNTIV TECHNOLOGIES INT. INC.
PI	Rattner JB, Yen TJ;
DR	WPI; 96-28711629.
DR	N-PSDB; T34578.
PT	DNA encoding kinetochore protein - used as a marker for the G2 and M phases of a cell cycle, partic. for detection of malignant diseases
PT	Claim 12; Page 41-54; 72pp; English.
CC	A 372 kDa human kinetochore protein, CENP-F (R99795), is detected by immunofluorescence microscopy only during the G2 and M phases of a cell cycle. It is the product of a cDNA clone (T34578) isolated from a breast carcinoma cDNA library. Recombinant CENP-F can be produced by expression in prokaryotic or eukaryotic host cells. CENP-F can be used to detect autoimmune antibodies to the protein, which may provide an early diagnosis for the onset

CC  
of various malignant diseases. Use of CENP-F as a cell cycle  
marker allows the specific detection of G2 and M phase cells.  
Sequence 3248 AA;

PI **Folkkes DM**, **Hoffman NJ**, **Kay BK**, **McConnell SJ**, **Sparks AB**  
 DR **WP**; **95 4505/546**.  
 DR **NPSDB**; **T39793**.

PI August PR, Flickinger MC, Sherman DH;  
 WPI 95-15267/720;  
 DR N-PSPB; Q87790.  
 PT Genes encoding resistance to DNA alkylating and cleavage agents  
     - used to combat drug resistance of tumour cells or as potential  
     anticancer agents  
 PS Disclosure; Fig 2.; 111P; English.  
 CC A 3.2 kb fragment from pDPS3003 including the *mcr* locus of *S.*  
 CC *lavendulae* B619 was cloned into pUC119 and sequenced. The locus  
     includes 3 coding sequences, *mcrA*, *mcrB* and *mcrORF3*. Both *mcrA* and  
     *B* are needed for high level resistance to mitomycin-C.  
 SQ Sequence 228 AA;

Query Match 3.6%; Score 103; DB 13; Length 228;  
 Best Local Similarity 29.1%; Pred. No 4.11e+01;  
 Matches 21; Mismatches 48; Indels 4; Gaps 4;

84 laeapcgaderprpaqgaalssrrsrirprbaaaaqatpraaerspaslaer 143  
| : | : | : | : | : | : | : | : | : | : | : |  
1 MAEPLURGRGPSSR-GGRGARRARGRCPRARQSARLIDTVLVDLVSDEEV-L-EV 58  
144 pgrrvaptar papatsspvggssgpltsaniarasapr 185  
| : | : | : | : | : | : | : | : | : | : |  
59 ADP-VEVPVARPPAPKEQDDSDSEGAEEQPGAPRTLYRR 100

RESULT	12
ID	W05393; standard; protein; 788 AA.
AC	W05393;
DT	19-FEB-1998 (first entry)
DE	Mouse SH3P12 protein.
KW	src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening; cell-cellular signal transduction process.
OS	Mus musculus.
PN	W0631625-A1.
PD	10-OCT-1996.
PF	04-APR-1995; U04454.
PR	03-APR-1996; US-630915.
PR	07-APR-1995; US-417872.
PA	(CITO-) CITOPEN CORP.
(UNNC-)	UNIV NORTH CAROLINA.

**KW**  
**Rubella; vaccine; mutant; epitope; virus; autoimmune disease;**  
**pregnancy; foetal infection; vector; plasmid.**  
**Rubella virus.**  
**US5433814-A.**  
**PN**  
**PD**  
**08-AUG-1995.**  
**PF**  
**28-JUN-1991.**  
**PR**  
**28-JUN-1991.**  
**PR**  
**19-JUL-1993.**  
**US 093453.**  
**(GEOR-) GEORGIA STATE RES FOUND INC.**  
**PI**  
**Dominguez G, Frey TK, Wang C;**  
**DR**  
**WPI ; 95-28309/737.**  
**N-PSSB;**  
**097686.**  
**PT**  
**New DNA encoding infectious rubella virus - esp. non-pathogen-**  
**mutant virus for use in vaccines having reduced side effects**  
**PS**  
**Disclosure; Columns 17-28; 21PP; English.**  
**CC**  
**Non-pathogenic mutants of the DNA corresponding to this sequence**  
**CC**  
**in vaccines (which may include epitopes from other viruses).**  
**CC**  
**The mutant vaccines are less likely to cause foetal infection or**  
**CC**  
**autoimmune disease or neurological symptoms, so can be administered**  
**safely to older or pregnant women. The mutant sequence is**

preferably present in a vector, especially a bacterial plasmid that allows replication of the sequence.

**Query Match** 3.5%; Score 102; DB 15; Length 2205; Best Local Similarity 33.3%; Pred. No. 4.71e+01; MS; Sequence 2205 AA;

Best Local Similarity 37%; Conservative 17; Mismatches 48; Indels 9; Gaps 7; FH

Matches 37; Conservatve 17; Mismatches 48; Indels 9; Gaps 7; FH

Db 2086 garpppgghrrragdssp-lraqsprlrltplygplilptlrssptvphlgvtq 2144  
QY 9 GPRRGRRGARRAGARGRCRPARSP-LIP--DT-VLWDYVSDSEEV-LEVADPV 62

Db 2145 l1pfgrapcpgpnqfyyphing-gpgeqprgtippargtirrrabapeaa 2194  
QY 63 EVPARLPAPAKPEQDSDSDSEGAAEGPAGA-PRTLVRRRRRLIDPGEP 112

**RESULT** 14 standard; Protein: 213 AA.

**ID** W14567; Standard: Protein; 213 AA.

**AC** W14567; 28-OCT-1997 (first entry)

**KW** Streptococcus pneumoniae PspA central region.

**OS** PspA; pneumococcal surface protein; vaccine; otitis media; meningitis; bacteraemia; pneumonia.

**KW** Streptococcus pneumoniae strain Ba8090.

**FT** Misc-difference 2 /note= "unidentified amino acid"

**FT** W0970999-A1.

**PD** 20-MAR-1997.

**PF** 16-SEP-1996; U14819.

**PR** 15-SEP-1995; US-52055.

**PA** (UABR) UAB RES FOND

**PI** Briles DE, Brooks Walter A, Crain MJ, Hollingshead S, McDaniel LS, Swiatlo E, Tart R, Yother J;

**DR** WPI; 97-202002/18.

**PT** Streptococcus pneumoniae surface protein PspC and truncated PspA - used in vaccines for protecting animals against S.pneumoniae infection

**PT** Example 6; Fig 13; 296PP; English.

This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain Ba8090. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine composition. 213 AA;

**Query Match** 3.5%; Score 99; DB 24; Length 213; Best Local Similarity 36.8%; Pred. No. 7.12e+01; MS; Matches 21; Conservatve 12; Mismatches 22; Indels 2; Gaps 2; FH

Db 148 daalnelnlgpdgdeetpapapakkeqpapapkpqepapapapk 204  
QY 41 DTVLYDLVSDSDEVLELEVADPVEVAPARLPAPA KPEQDSDSDSEGAAE-GPACAPR 95

**RESULT** 15 standard; Protein: 386 AA.

**ID** W18664; AC W18664; DT 24-JUL-1997 (first entry)

**DE** Fragmented human NF-H gene +1 frameshift mutant product.

**KW** Frameshift mutation product; GAGA motif; somatic mutation; diagnosis; detection; antibody; probe; cancer; neoplasia; neurodegenerative; Parkinson's; Alzheimer's disease; Pick's; Huntington's disease;

**KW** Down's syndrome; frontal lobe dementia; progressive supranuclear palsy; PSP; amyotrophic lateral sclerosis; multiple sclerosis; MS; cardiovascular; rheumatoid arthritis.

**OS** Homo sapiens.

**FT** Key misc-difference 1.387 /note= "X corresponds to a stop codon in the accompanying DNA file, T69796."

**FT** peptide 120..135 /note= "antigenic peptide used fro antibody production"

**FT** FTN W09712992-A2.

**FT** PD 10-APR-1997.

**FT** PR 02-OCT-1995; GB-020080.

**FT** PR 11-JAN-1996; US-008832.

**PR** PA (ROYAL) ROYAL NETHERLANDS ACAD ARTS & SCI.

**PA** (UVR-) UNIV ROTTERDAM ERASMUS.

**PI** Burbach JPH, Grosvenor FG, van Leeuwen FW;

**DR** WPI; 97-226235/20.

**PT** N-PSB; T69796 use of mutant genes having frame-shift mutation(s) - for developing prods. for the diagnosis, prevention and treatment of associated diseases, e.g. cancer or neuro-degenerative disease

**PT** PS Claim 22; Fig 9; 123PP; English.

**CC** W18663 and W18664 are +2 and +1 frameshift mutations, respectively, of a sequence comprising fragments of the coding sequence of the human neurofilament subunit NF-H gene corresponding to nucleotides 1-1162 of the wild-type NF-H gene. This region contains GAGAG motifs.

**CC** Frame-shift mutants of the tau, ubiquitin, apolipoprotein E, microtubule-associated protein 2 (MAP-2), neurofilament subunit L, M and H and amyloid A4 genes are claimed. All these genes share a common GA/GAG motif (N=A, G, C or T), which is the site of common GA dinucleotide deletion(s) that cause neurodegenerative disorders.

**CC** Antigenic peptides used for the production of antibodies, and small nucleic acid sequences derived from frame-shift mutants are used in the diagnosis, prevention and treatment of cancer and neurodegenerative diseases, e.g. Parkinson's disease, Alzheimer's disease, Down's syndrome, frontal lobe dementia (Pick's disease), progressive supranuclear palsy (PSP), amyotrophic lateral sclerosis, Huntington's disease, multiple sclerosis, and other degenerative diseases such as cardiovascular disease and rheumatoid arthritis.

**CC** Sequence 386 AA;

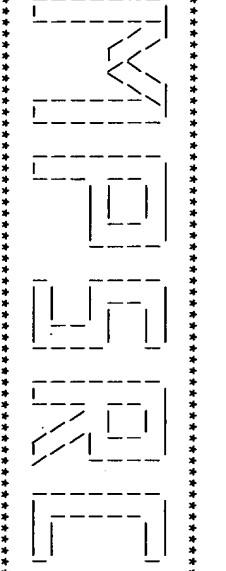
**Query Match** 3.5%; Score 100; DB 22; Length 386; Best Local Similarity 55.2%; Pred. No. 6.21e+01; MS; Matches 16; Conservatve 6; Mismatches 5; Indels 2; Gaps 2; FH

Db 231 Plrygravarrqprdarq-aaprgars 258  
QY 4 PLR-GRGPRSGRGARRAGARGRCRA 31

Search completed: Fri Feb 18 11:57:17 2000  
Job time : 94 secs.

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MPSPCH\_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Feb 18 12:02:02 2000; MasPar time 7.55 Seconds

705.764 Million cell updates/sec

cular output not generated.

Title:

Description: >US-08-755-584-2  
(1-412) from 5858711.pep

Perfect Score:

Sequence: 1 MAEPLGRGRPRSRKGRR... . . . . . GKELPADLGSQDLIEWNG 412

Scoring table: PAM 150

Gap 11

Searched: 131253 seqs, 12056647 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-issued

1:5A..COMB 2:5B..COMB 3:PCT9..COMB 4:backfiles1

Statistics: Mean 32.940; Variance 177.353; scale 0.186

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	Pred. No.
1	2858	100.0	412	2 US-08-755- Sequence 2, Application 2.34e+214	24
2	160	50.0	104	2 US-08-853- Sequence 3, Application 4.58e-03	25
3	152	5.3	126	2 US-08-853- Sequence 1, Application 1.57e-02	26
4	113	4.0	673	2 US-08-455- Sequence 6, Application 5.18e+00	27
5	105	3.7	265	2 US-08-970- Sequence 1, Application 1.38e+01	28
6	107	3.7	3248	3 PCT-U595-1. Sequence 1, Application 1.21e+01	29
7	107	3.7	3248	1 US-08-353- Sequence 1, Application 1.21e+01	30
8	102	3.6	210	1 US-08-093- Sequence 2, Application 2.44e+01	31
9	100	3.5	181	2 US-08-726- Sequence 56, Application 3.21e+01	32
10	99	3.5	397	3 PCT-U596-1. Sequence 6, Application 3.69e+01	33
11	99	3.5	568	3 PCT-U594-0. Sequence 30, Application 3.69e+01	34
12	99	3.5	1	US-08-320- Sequence 30, Application 3.69e+01	35
13	98	3.4	30	1 US-08-218- Sequence 10, Application 4.23e+01	36
14	97	3.4	123	2 US-08-306- Sequence 5, Application 4.85e+01	37
15	97	3.4	2	US-08-240- Sequence 1, Application 4.88e+01	38
16	97	3.4	166	1 US-07-935- Sequence 2, Application 4.85e+01	39
17	97	3.4	166	1 PCT-U593-0. Sequence 2, Application 4.85e+01	40
18	97	3.4	166	1 US-08-368- Sequence 2, Application 4.85e+01	41
19	98	3.4	237	2 US-08-970- Sequence 5, Application 4.23e+01	42
20	97	3.4	359	2 US-09-092- Sequence 6, Application 4.85e+01	43
21	96	3.4	359	2 US-08-802- Sequence 3, Application 5.55e+01	44
22	96	3.4	389	2 US-08-802- Sequence 14, Application 4.85e+01	45
23	97	3.4	US-09-092-	Sequence 3, Application 4.85e+01	46

ALIGNMENTS

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX
DT	XX	XX	XX	XX	XX
AC	XXXXX	XXXXX	XXXXX	XXXXX	XXXXX
XX	XX	XX	XX	XX	XX

ID	RESULT	1	STANDARD	PERT	412 AA.
XX	XX	XX	XX	XX	XX

CC MOLECULE TYPE: protein  
 CC TOPLOGIC: linear  
 CC SOURCE: 412 AA; 45121 MW; 892836 CN;  
 CC Query Match 100 %; Score 2858; DB 2; Length 412;  
 CC Best Local Similarity 100 %; Pre. No. 2,34e-214;  
 CC Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 Db 1 MAEPLRGRGPRSGRGARRARGRCPRAROSPARLIPDYLVDLVSDEEVLEVAD 60  
 Qy 1 MAEPLRGKGPRSGRGARRARGRCPRAROSPARLIPDYLVDLVSDEEVLEVAD 60  
 Db 61 PHEPVVARLPAPAKPEQDSDSSEGAAEGPAGAPRLVRRRLIDPGEARPVVPTYSGK 120  
 Qy 61 PVEPVVARLPAPAKPEQDSDSSEGAAEGPAGAPRLVRRRLIDPGEARPVVPTYSGK 120  
 Db 121 VVSSLNLIPDNSSLKLCPSEPERDEADLNTNSGSSPSDDALPSGSWPKRKCCKEEK 180  
 Qy 121 VVSSLNLIPDNSSLKLCPSEPERDEADLNTNSGSSPSDDALPSGSWPKRKCCKEEK 180  
 Db 241 DENVTLVSPQIQLQSSRFLTIRCRADLVRLIVRMSPLQNYDMDHANLGVSPNILL 300  
 Qy 241 DENVTLVSPQIQLQSSRFLTIRCRADLVRLIVRMSPLQNYDMDHANLGVSPNILL 300  
 Db 301 FGSELSPLSTPLSKLGAVDITDCVVLASSEATETSQELRLRVGKKEHQMLTSLSP 360  
 Qy 301 FGSELSPLSTPLSKLGAVDITDCVVLASSEATETSQELRLRVGKKEHQMLTSLSP 360  
 Db 361 DSPLKVLMHSYEEAMGLSGHKLISFEEGTKLKGELPADLGSQLEGLIEWNG 412  
 Qy 361 DSPLKVLMHSYEEAMGLSGHKLISFEEGTKLKGELPADLGSQLEGLIEWNG 412

**RESULT**  
 ID US-08-853-974-3 STANDARD; PRT; 104 AA.  
 XX  
 AC XXXXX  
 DT XX  
 DE Sequence 3, Application US/08853974  
 Sequence 3, Application US/08853974  
 Patent No. 5840334  
 GENERAL INFORMATION:  
 APPLICANT: Shah, Purvi  
 TITLE OF INVENTION: HUMAN SMT3-LIKE PROTEIN  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304

**COMPUTER READABLE FORM:**  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/853-974  
 FILING DATE: Filed Herewith  
 PRIORITY DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PFR-0289 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-845-4166  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 104 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CC  
 CC CC CC CC CC CC CC CC CC CC  
 CC CC CC CC CC CC CC CC CC CC  
 CC CC CC CC CC CC CC CC CC CC  
 CC CC CC CC CC CC CC CC CC CC  
 SQ SEQUENCE 104 AA; 11654 MW; 46917 CN;  
 Query Match 5.6%; Score 160; DB 2; 1st  
 Best Local Similarity 25.7%; Pred. No. 4.58e-03;  
 Matches 19; Conservative 26; Mismatches 28;  
 Matches 19; Conservative 26; Mismatches 28;  
 Db 13 DSGGAHINLKVKGODGNEYF-FRIKRSTQKLKLMAYCDDQSVDH  
 : : : | : | :  
 QY 336 ETSOELRLRVQGKEKHOMLEISLSPDSDLPLVLMHVEAMGLSC  
 Db 72 TDDELDMEDGEDEID 85  
 Qy | : | : | : | :  
 396 LPADIGLGESGLIE 409

RESULT	3
ID	US-08-053-974-1
XX	STANDARD;
AC	xxxxxx
XX	
DT	
XX	
DE	
Sequence 1, Application US/08853974	
Sequence 1, Application US/08853974	
Patent No. 5840534	
GENERAL INFORMATION:	
APPLICANT: Billman, Jennifer L.	
APPLICANT: Shah, Purvi	
TITLE OF INVENTION: HUMAN SMT3-LIKE PROTEIN	
NUMBER OF SEQUENCES: 3	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Incyte Pharmaceuticals, Inc.	
STREET: 3174 Porter Drive	
CITY: Palo Alto	
STATE: CA	
COUNTRY: USA	
ZIP: 94304	
COMPUTER READABLE FORM:	
COMPUTER: IBM Compatible	
MEDIUM TYPE: Diskette	
OPERATING SYSTEM: DOS	
SOFTWARE: FASTSEQ FOR Windows Version 2.0	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/053,974	
FILING DATE: Filed Herewith	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	
FILING DATE:	
ATTORNEY/AGENT INFORMATION:	
NAME: Billings, Lucy J.	
REGISTRATION NUMBER: 36,749	
REFERENCE/DOCKET NUMBER: PFR-0289 US	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 415-845-0555	
TELEFAX: 415-845-4166	
INFORMATION FOR SEQ ID NO: 1:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 126 amino acids	

TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: LUNGFET03  
 CLONE: 2361410  
 SEQUENCE 126 AA; 13961 MW; 87522 CN;

Query Match 5.3%; Score 152; DB 2; Length 126;  
 Best Local Similarity 31.6%; Pred. No. 1.57e-02; Mismatches 19; Indels 33; Gaps 2;  
 Matches 25; Conservative 19; Mismatches 33; Indels 2; Gaps 2;

Db 8 EGVTENDHINKVAGQDS-VVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFPFDGQPI 66  
 Qy || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 333 EATTSQE-LRLRVGKERHQMLISLSPDSPLKVLMSHYEANGLSCHKLSPFDGTLK 391

Db 67 NETHTPAQLEMEDDTIDV 85  
 Qy : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 392 SGKELPADIGLESQDILV 410

BUILT 4 US-08-475-073A-6 STANDARD: PRT: 673 AA.  
 XX DE RESULT 5 ID US-08-970-133-1 STANDARD: PRT: 265 AA.  
 AC XX ID XX  
 XX AC XXXXXX DT XX  
 XX DE Sequence 1, Application US/08970133  
 CC XX Sequence 1, Application US/08970133  
 CC XX Patent No. 5916753  
 CC GENERAL INFORMATION: GENERAL INFORMATION:  
 CC APPLICANT: Bandman, Olga  
 CC APPLICANT: Gideon Dreyfuss  
 CC APPLICANT: Mikiko C. Sionil  
 CC APPLICANT: Yan Zhang  
 CC TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods  
 CC TITLE OF INVENTION: Of Making And Using The Same  
 CC NUMBER OF SEQUENCES: 13  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 CC STREET: 3174 Porter Dr.  
 CC CITY: Palo Alto  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 94304  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Diskette  
 CC COMPUTER: IBM Compatible  
 CC OPERATING SYSTEM: DOS  
 CC SOFTWARE: FastSEO for Windows Version 2.0  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/970,133  
 CC FILING DATE: Filed Herewith  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER:  
 CC FILING DATE:  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Billings, Lucy J.  
 CC REGISTRATION NUMBER: 36,749  
 CC REFERENCE/DOCKET NUMBER: PP-0419 US  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 650-555-0555  
 CC TELEFAX: 650-845-4166  
 CC INFORMATION FOR SEQ ID NO: 1:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 265 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC IMMEDIATE SOURCE:  
 CC LIBRARY: BRAITU03  
 CC CLONE: 863744  
 SQ SEQUENCE 265 AA; 30106 MW; 347009 CN;

Query Match 3.7%; Score 106; DB 2; Length 265;  
 Best Local Similarity 28.6%; Pred. No. 1.39e-01; Mismatches 21; Indels 4; Gaps 4;  
 Matches 22; Conservative 21; Mismatches 30; Indels 4; Gaps 4;

Db 38 NGKATPEDTSNLPP-EQRKRLQOKVDELKEIQLKEMDORDATAKMKDVYLNQMGDA 95  
 Qy || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 150 NSGSSPSEDDALPSGPSPWRKLRKCEKEKKME-EFFQDQ-ISPLPQPSRNKRKITE 207

Query Match 4.0%; Score 113; DB 2; Length 673;  
 Best local similarity 32.4%; Pred. No. 5.18e-00; Mismatches 18; Indels 4; Gaps 4;  
 Matches 23; Conservative 18; Mismatches 26; Indels 4; Gaps 4;

Db 97 SDLKLAEVQSONTEKLR 113  
 : | : | : | : | : | : |



APPLICANT: FREY, Teryl K.  
 CC APPLICANT: Dominguez, Geraldina  
 CC APPLICANT: Wang, Chin-Yen  
 CC TITLE OF INVENTION: Modified Infectious Rubella Virus  
 CC NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Jamie L. Greene, Jones & Askew  
 CC STREET: 191 Peachtree Street, 37th Floor  
 CC CITY: Atlanta  
 CC STATE: Georgia  
 CC COUNTRY: United States  
 CC ZIP: 30303  
 COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Diskette, 3.50  
 CC COMPUTER: Macintosh  
 CC OPERATING SYSTEM: 7.0  
 CC SOFTWARE: Microsoft Word  
 CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/093,453B  
 CC FILING DATE: 19 JUL 1993  
 CC CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: U.S. 07/722,334  
 CC FILING DATE: 28 JUN 1991  
 ATTORNEY/AGENT INFORMATION:  
 CC NAME: Greene, Jamie L.  
 CC REGISTRATION NUMBER: 32,467  
 CC REFERENCE/DOCKET NUMBER: 07362-0101  
 TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 404-818-3799  
 CC TELEFAX: 404-818-3799  
 INFORMATION FOR SEQ ID NO: 2:  
 CC SEQUENCE CHARACTERISTICS:  
 LENGTH: 2205 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE: Ribella virus  
 ORGANISM: Ribella virus  
 CC STRAIN: Therien  
 CC SEQUENCE 2205 AA; 240235 MW; 2250019 CN;  
 Query Match 3, 5%; Score 102; DB 1; Length 2205;  
 Best Local Similarity 33.3%; Pred. No. 2.44e-01;  
 Matches 37; Conservative 17; Mismatches 48; Indels 9; Gaps 7;  
 CC SEQUENCE 181 AA; 17613 MW; 98529 CN;  
 Query Match 3, 5%; Score 100; DB 2; Length 181;  
 Best Local Similarity 55.2%; Pred. No. 3.21e-01;  
 Matches 16; Conservative 6; Mismatches 5; Indels 2; Gaps 2;  
 CC SEQUENCE 181 AA; 17613 MW; 98529 CN;  
 Query Match 3, 5%; Score 100; DB 2; Length 181;  
 Best Local Similarity 55.2%; Pred. No. 3.21e-01;  
 Matches 16; Conservative 6; Mismatches 5; Indels 2; Gaps 2;  
 CC SEQUENCE 181 AA; 17613 MW; 98529 CN;  
 RESULT 9 ID PCT-US96-10602-6 STANDARD; PRT; 397 AA.  
 ID US-08-726-306A-56 DT PCT-US96-10602-6 STANDARD; PRT; 397 AA.  
 XX AC xxxxxx  
 CC Sequence 6, Application PC/TUS9610602  
 CC GENERAL INFORMATION:  
 CC APPLICANT: The General Hospital Corporation  
 CC TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION  
 CC NUMBER OF SEQUENCES: 14  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Fish & Richardson P.C.  
 CC STREET: 225 Franklin Street  
 CC CITY: Boston  
 CC STATE: MA  
 CC COUNTRY: USA  
 CC ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

APPLICANT: Grosveld, Franklin G.  
 CC TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS  
 CC NUMBER OF SEQUENCES: 189  
 CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Banner & Witcoff, Ltd.  
 CC STREET: 1 Financial Center  
 CC CITY: Boston  
 CC STATE: MA  
 CC COUNTRY: US  
 CC ZIP: 02111  
 COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: WordPerfect 6.1  
 CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/726,306A  
 CC FILING DATE: 02-oct-1996  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: GB 95/20080.4  
 CC FILING DATE: 02-oct-1995  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: US 60/009,832  
 CC FILING DATE: 01-Jan-1996  
 ATTORNEY/AGENT INFORMATION:  
 CC NAME: Williams, Ph.D., Kathleen M.  
 CC REGISTRATION NUMBER: 34,380  
 CC REFERENCE/DOCKET NUMBER: 96-048-A (3255/00784)  
 TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (617) 345-9100  
 CC TELEFAX: (617) 345-9111  
 INFORMATION FOR SEQ ID NO: 56:  
 CC SEQUENCE CHARACTERISTICS:  
 LENGTH: 181 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPLOGY: unknown  
 MOLECULE TYPE: peptide  
 CC SEQUENCE 181 AA; 17613 MW; 98529 CN;

Query Match 3, 5%; Score 100; DB 2; Length 181;  
 Best Local Similarity 55.2%; Pred. No. 3.21e-01;  
 Matches 16; Conservative 6; Mismatches 5; Indels 2; Gaps 2;  
 CC SEQUENCE 181 AA; 17613 MW; 98529 CN;  
 Db 42 PLRGRAVRRGPRDARG-AAPGRGARS 69  
 QY 4 PLR-GRGRGGGARRGARRGRCRA 31  
 RESULT 10 ID PCT-US96-10602-6 STANDARD; PRT; 397 AA.  
 ID US-08-726-306A-56 DT PCT-US96-10602-6 STANDARD; PRT; 397 AA.  
 XX AC xxxxxx  
 CC Sequence 6, Application PC/TUS9610602  
 CC GENERAL INFORMATION:  
 CC APPLICANT: The General Hospital Corporation  
 CC TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION  
 CC NUMBER OF SEQUENCES: 14  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Fish & Richardson P.C.  
 CC STREET: 225 Franklin Street  
 CC CITY: Boston  
 CC STATE: MA  
 CC COUNTRY: USA  
 CC ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

Sequence 56, Application US/08726306A  
 DE Sequence 56, Application US/08726306A  
 XX Patent No. 5958684  
 AC GENERAL INFORMATION:  
 CC APPLICANT: van Leeuwen, Frederik Willem  
 CC APPLICANT: Burbach, Johannes Peter Henrili





**RESULT** 64 VPVARLPPAKPEQEDSDSDSEGAAEGPAGPRTLVRRR 102  
**ID** US-08-240-717A-1    **STANDARD:** PRT; 123 AA.  
**XX**  
**XX**  
**AC**  
**XX**  
**XX**  
**DT**  
**DE** Sequence 1, Application US/08240717A  
**CC** Sequence 1, Application US/08240717A  
**CC** Patent No. 5965353  
**CC** GENERAL INFORMATION:  
**CC** APPLICANT: Middendorp, Jaap M.  
**CC** TITLE OF INVENTION: Epstein Barr Virus Peptides and  
**CC** TITLE OF INVENTION: Antibodies Against These Peptides  
**CC** NUMBER OF SEQUENCES: 6  
**CC** CORRESPONDENCE ADDRESS:  
**CC** ADDRESSEE: Akzo No. 5965353 el Patent Dept.  
**CC** STREET: 1300 Piccard Drive, Suite 206  
**CC** CITY: Rockville  
**CC** STATE: Maryland  
**CC** COUNTRY: US  
**CC** ZIP: 20850  
**CC** COMPUTER READABLE FORM:  
**CC** MEDIUM TYPE: Floppy disk  
**CC** COMPUTER: IBM PC compatible  
**CC** OPERATING SYSTEM: PC-DOS/MS-DOS  
**CC** SOFTWARE: Patent Release #1.0, Version #1.30  
**CC** CURRENT APPLICATION DATA:  
**CC** APPLICATION NUMBER: US/08/240,717A  
**CC** FILING DATE: 11-MAY-1994  
**CC** CLASSIFICATION: 435  
**CC** PRIOR APPLICATION DATA:  
**CC** APPLICATION NUMBER: EP 92 202797 4  
**CC** FILING DATE: 14-SEP-1992  
**CC** ATTORNEY/AGENT INFORMATION:  
**CC** NAME: Gormley, Mary E.  
**CC** REGISTRATION NUMBER: 34,409  
**CC** TELEPHONE: (301) 258-5200  
**CC** TELEFAX: (301) 977-0847  
**CC** INFORMATION FOR SEQ ID NO: 1:  
**CC** SQUENCE CHARACTERISTICS:  
**CC** LENGTH: 123 amino acids  
**CC** TYPE: amino acid  
**CC** STRANDEDNESS: single  
**CC** TOPOLOGY: linear  
**CC** MOLECULE TYPE: peptide  
**SQ** SEQUENCE 123 AA; 12990 MW; 70971 CN;  
  
**Query Match** 3.4%; Score 97; DB 2; Length 123;  
**Best Local Similarity** 28.3%; Pred. No. 4.8e+01;  
**Matches** 28; Conservative 26; Mismatches 38; Indels 7; Gaps 63  
  
**Db** 21 RARG-RGKG-RQEKRPSPSSQSSSSGSPPRRPPGRRFFFHVGREADYFEHQEGGPDG 78  
**Db** 6 RGRGPSPRSRGRCARRANGRGCPRAQSPLRIPD-WLVLDVSDSE-EVLEVAIDPV 63  
**Db** 79 EP-D-VPGATEQGPADDPGEPSGTGPKQGDG-GRRK 114  
**Dy** 64 VPVARLPPAKPEQEDSDSDSEGAAEGPAGPRTLVRRR 102

Search completed: Fri Feb 18 12:02:29 2000  
Job time : 27 secs.



#title Identification and characterization of the SMT3 cDNA and gene  
from nematode *Caenorhabditis elegans*.  
#cross-references MUID:97318858  
#accession JCS582  
##molecule\_type DNA  
#residues 1-91 #label CHO  
COMMENT This protein is a suppressor of MIF2 mutation in a centromere protein.  
GENETICS  
#gene smt3  
#introns 22/3; 5/2  
CLASSIFICATION #superfamily yeast SMT3 protein  
#length 91 #molecular-weight 10222 #checksum 2101  
SUMMARY  
Query Match 5.3%; Score 152; DB 2; Length 91;  
Best Local Similarity 22.5%; Pred. No. 2.96e-05;  
Matches 18; Conservative 31; Mismatches 30; Indels 1; Gaps 1;  
Db 5 AAQAGDNAYIKKVVGODSNEV-HFRVKYIGSMMAKUKSYADRGTGVAVNSURFLDGR 63  
Oy 331 SSEATTSOELURVDOKEKHOMELISLSPDPLKVLMHYEAMGLSGHKLSFFDGTC 390  
Db 64 INDDDTPTLEEDDDIEV 83  
Oy 391 LSGKELPADGLGESGDIEV 410  
RESULT 3  
ENTRY I46707 #type complete  
TITLE Initiation factor 4-gamma - rabbit  
ORGANISM #formal\_name Oryctolagus cuniculus #common\_name domestic  
RABBIT  
DATE 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change  
14-Feb-1997  
ACCESSIONS  
REFERENCE  
#authors Yan, R.; He, W.; Rhoads, R.E.  
#journal J. Biol. Chem. (1993) 268:19200-19203  
#title Mapping the cleavage site in protein synthesis initiation  
factor eif-4 gamma of the 2A proteases from human  
Coxackievirus and rhinovirus.  
#cross-references MUID:9374895  
#accession I46707  
#status Preliminary; translated from GB/EMBL/DDJB  
##molecule-type mRNA  
##residues 1-1402 #label YAN  
#cross-references GB:L12290; NID:9404774; PID:9404775  
#length 1402 #molecular-weight 154049 #checksum 1846  
SUMMARY  
Query Match 4.5%; Score 129; DB 2; Length 1402;  
Best Local Similarity 20.8%; Pred. No. 1.5e-02;  
Matches 46; Conservative 62; Mismatches 103; Indels 10; Gaps 10;  
Db 482 ALSSRGPRGGPGGEPLPRAAGLGPRESLQRPPKGARKLTASVIMTEDIRLNKAKAW 540  
Oy 4 PRGRGRFRSRGGRRARGARGRCPRARQSFLRFLTVLVLVSDSDEEVLEVADPVE 63  
Db 541 KISSKRPAAKD-DR-GEDDADESKTDLFLRRYRSILKLTPMPFQOLMKVQIQLAIDTEG 598  
Oy 64 VEVVARLPAPAKPQQDSDSEGAA-EAEGPAGAPRTLVRRRLIDPGEAPVPPV-VSGKV 121  
Db 599 ASKGSLTSSLRPPONITSONWSQHVLPHGAEATREKPTIVN-FRKLLNRCQKEFE 657  
Oy 122 OSSSLNLIPDNSSLKLKLPSE-PEDDEADLNTNSSSPSDDALPSGSPWPKLKKCEKE-E 179  
Db 658 KOKDDEDEVFEKKQEMDEATEERERIKEELFEEARDTARR 698  
Oy 180 K-KME-BFPQDISPLQPOPSSRNKRKRTEALQKLREVNR 218  
GENETICS  
#gene Rv369  
SUMMARY  
#length 771 #molecular-weight 81409 #checksum 4348  
RESULT 4  
ENTRY 563999 #type complete



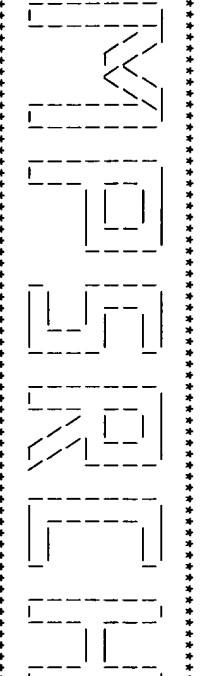
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#journal Nature Genet. (1993) 3:137-145
#title Dense HLA cluster and a Potential new member of the
#organism NFKappaB family within a 90 kilobase HLA class III segment.
#accession S36152
#status preliminary
##molecule_type DNA
##residues 1-1872 ##label IRI
##cross-references EMBL:215225
##note in the authors' translation residues 32-34 are shown
#note after residue 4 and, consequently, residues 5-31 are
#note displaced three codons to the right.
#note the authors translated the codon AAT for residue 1000 as
#note His
#GENETICS
#introns 38/2; 97/2; 129/3; 154/1; 202/1; 252/3; 279/2; 327/1; 357/2;
#length 1872 #molecular-weight 199338 #checksum 7324
#note best local similarity 29.5%; pred. no. 5.31e-01; mismatches 31; conservative 31; indels 6; gaps 6;
#note Query Match 4.0%; score 115; DB 2; length 1872;
#note Best Local Similarity 29.5%; Pred. No. 5.31e-01; Mismatches 37; Indels 6; Gaps 6;
#note Matches 31; Conservative 31; Indels 6; Gaps 6;
#note Qy 65 PVALAPAPKPEODSDSEGAAGPAGAPRILVRR-RRRLLDP 1080
#note Db 1024 RGRGTYFARG-RGRGTYGGRGRGQANSAVTEFEEMMCGVE-VGQGDQTTLIFEEA-M 1068
#note Qy 6 RGRGP-RSGRGGRARRGARGPRARSPARIPDVTLYLDSDEBELEVADPVY 64
#note Db 1081 P-ARHGVYOSMRKSPGAGSGAKQQAARPMRVTLQTLRRLPP 1124
#note Qy 65 PVALAPAPKPEODSDSEGAAGPAGAPRILVRR-RRRLLDP 108
#note
#note RESULT 10
#note ENTRY B35098 #type complete
#note TITLE MHC class III histocompatibility antigen HLA-B-associated
#note ORGANISM Homo sapiens #common_name man
#note DATE 10-Aug-1990 #sequence_revision 06-Nov-1992 #text_change
#note ACCESSIONS B35098
#note REFERENCE Bareril, J.; Sands, J.; Strominger, J.L.; Spies, T.
#note #authors Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2374-2378
#note #title A gene pair from the human major histocompatibility complex
#note encodes large proline-rich proteins with multiple repeated
#note motifs and a single ubiquitin-like domain.
#note #cross-references MUID:90192810
#note #accession B35098
#note #status preliminary
#note ##molecule_type mRNA
#note ##residues 1-2142 ##label BAN
#note ##cross-references GB:M33509; NID:9179338; PID:9179339; GB:M31293
#note ##note the authors translated the codon AGT for residue 97 as
#note Gly
#note #length 2142 #molecular-weight 227840 #checksum 5704
#note #SUMMARY
#note Query Match 4.0%; Score 113; DB 2; Length 2142;
#note Best Local Similarity 29.5%; Pred. No. 8.63e-01; Mismatches 31; Conservative 31; Indels 6; Gaps 6;
#note Matches 31; Conservative 31; Mismatches 38; Indels 6; Gaps 6;
#note Qy 65 PVALAPAPKPEODSDSEGAAGPAGAPRILVRR-RRRLLDP 108
#note Db 1024 RGRGTYFARG-RGRGTYGGRGRGQANSAVTEFEEMMCGVE-VGQGDQTTLIFEEA-M 1068
#note Qy 6 RGRGP-RSGRGGRARRGARGPRARSPARIPDVTLYLDSDEBELEVADPVY 64
#note Db 1069 P-ARHGVYOSMRKSPGAGSGAKQQAARPMRVTLQTLRRLPP 1112
#note Qy 65 PVALAPAPKPEODSDSEGAAGPAGAPRILVRR-RRRLLDP 108
#note
#note RESULT 12
#note ENTRY S11034 #type complete
#note TITLE gene P1 protein - fruit fly (Drosophila melanogaster)
#note ORGANISM #formal_name Drosophila melanogaster
#note DATE 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change
#note ACCESSIONS S11034
#note REFERENCE S11034
#note #authors Maschatt, F.; Dubertret, M.L.; Therond, P.; Claverie, J.M.; Lepesant, J.A.
#note #journal J. Mol. Biol. (1990) 214:359-372
#note #title Structure of the ecdysone-inducible P1 gene of Drosophila
#note #cross-references MUID:90339481
#note #accession S11034
#note #status preliminary
#note ##molecule_type DNA
#note ##residues 1-1030 ##label MAS
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#note GENETICS
#note #status preliminary
#note #cross-references EMBL:215225
#note #accession 151734
#note #status preliminary
#note #molecule_type DNA
#note #residues 1-1872 ##label IRI
#note ##cross-references EMBL:215225
#note #note the authors translated the codon AAT for residue 1000 as
#note His
#note #GENETICS
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1021/1; 1022/1; 1023/1; 1024/1; 1025/1; 1026/1; 1027/1; 1028/1; 1029/1; 1030/1; 1031/1; 1032/1; 1033/1; 1034/1; 1035/1; 1036/1; 1037/1; 1038/1; 1039/1; 1030/1; 1031/1; 1032/1; 1033/1; 1034/1; 1035/1; 1036/1; 1037/1; 1038/1; 1039/1; 1040/1; 1041/1; 1042/1; 1043/1; 1044/1; 1045/1; 1046/1; 1047/1; 1048/1; 1049/1; 1040/1; 1041/1; 1042/1; 1043/1; 1044/1; 1045/1; 1046/1; 1047/1; 1048/1; 1049/1; 1050/1; 1051/1; 1052/1; 1053/1; 1054/1; 1055/1; 1056/1; 1057/1; 1058/1; 1059/1; 1050/1; 1051/1; 1052/1; 1053/1; 1054/1; 1055/1; 1056/1; 1057/1; 1058/1; 1059/1;
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Search completed: Fri Feb 18 11:58:20 2000  
Job time : 45 secs.

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protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Feb 18 11:58:36 2000; MasPar time 13.08 Seconds

Unusual output not generated.

Title: >US-08-755-584-2

Description: (1-412) from 5858711.pep

PerfScore: 2858

Sequence: 1 MAEPLRGRGPRSRGGRARR.....GKELPADLGLLEGDLIEVG 412

Scoring table: PAM 150

Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% summaries

Listing first 45 summaries

Database: swissprot37  
1:swissprot

Statistics:  
Mean 50.879; Variance 107.959; scale 0.471  
  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	161	5.6	95	1	SM32_HUMAN	UBIQUITIN-LIKE PROTEIN
2	159	5.6	100	1	SM32_ORF3	UBIQUITIN-LIKE PROTEIN
3	160	5.6	104	1	SM32_ARATH	UBIQUITIN-LIKE PROTEIN
4	152	5.3	91	1	SM32_CAEEL	UBIQUITIN-LIKE PROTEIN
5	149	5.2	101	1	SM32_HUMAN	UBIQUITIN-LIKE PROTEIN
6	141	4.9	103	1	SM31_HUMAN	UBIQUITIN-LIKE PROTEIN
7	129	4.5	1402	1	FAAG_RABIT	EUKARYOTIC TRANSLATION
8	126	4.4	90	1	SM32_SCOPH	UBIQUITIN-LIKE PROTEIN
9	125	4.4	101	1	SM32_YEAST	UBIQUITIN-LIKE PROTEIN
10	113	4.0	673	1	FXK2_HUMAN	FRAGILE X MENTAL RETAR
11	2142	1	2142	1	BAT2_BRUAR	LARGE PROLINE-RICH PRO
12	111	3.9	359	1	IS12_BRUAR	INSULIN GENE ENHANCER
13	112	3.9	454	1	VE2 HPV37	REGULATORY PROTEIN E2
14	112	3.9	707	1	RHO_STRLKE	TRANSCRIPTION TERMINAT
15	111	3.9	1030	1	FAT-BODY	PROTEIN-1 PRE
16	108	3.8	229	1	V33P_ADP05	33 KD PHOSPHOPROTEIN
17	110	3.8	267	1	RS2_DROME	40S RIBOSOME
18	109	3.8	340	1	IS2B_ONC1S	ADENYL CYCLASE, TYP
19	110	3.8	385	1	GCH2_AZOB	MULTIDRUG RESISTANCE P
20	109	3.8	431	1	ULG1_HCAV4	POLYPROTEIN (253
21	110	3.8	476	1	VL2 HPV32	HYPOTHETICAL PROTEIN U
22	109	3.8	619	1	BCHD_CHIVI	MINOR CAPSID PROTEIN L
23	110	3.8	657	1	LAMA_CHICK	MAGNESIUM-CHELATASE

#### ALIGNMENTS

RESULT	ID	1	HUMAN	STANDARD;	PRT;	95 AA.
	AC	P55825:				
	DT	01-NOV-1997 (REL. 35, CREATED)				
	DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)				
	DE	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)				
	GN	UBIQUITIN-LIKE PROTEIN SMT3B (SENTINIL 2).				
	OS	SMT3H2 OR SMT3B.				
	OC	HOMO SAPiens (HUMAN), AND BOS TAURIS (BOVINE)				
	OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUROTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.				
	RN	[1]				
	RP	SEQUENCE FROM N.A.				
	RC	SPECIES=HUMAN; TISSUE=BRAIN;				
	RX	LAPENZA V., CHURAZZI P., VAN DER SPEK P.J., PIZZUTI A., HANADA F., BRAHE C.;				
	RX	"SM32, a human homologue of the <i>S. cerevisiae</i> Smr3 gene, maps to chromosome 21qter and defines a novel gene family.";				
	RL	GENOMICS 40:362-367(1997).				
	RN	[2]				
	RP	SEQUENCE FROM N.A.				
	RC	SPECIES=Bovine; TISSUE=ENDOMETRIUM;				
	RA	OJ F., BERRY E.S.;				
	RA	UBIQUITIN-LIKE PROTEIN				
	RL	SUBMITTED (MAR 1997) TO EMBL/GENBANK/DDBJ DATA BANKS.				
	CC	-1 SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.				
	CC					
	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
	CC					
	CC					
	DR	X99885; E74602; -;				
	DR	EMBL: U89439; G188536; -.				
	DR	MIM: 603042; -;				
	DR	PROSITE: PS5003; UBIQUITIN_2; 1.				
	FT	DOMAIN 15 95 UBIQUITIN-LIKE.				
	SQ	SEQUENCE 95 AA: 10871 NW; E49F30B9 CRC32;				

#### Query Match

Score 161; DB 1; Length 95;

Best Local Similarity 32.9%; Pred. No. 8.16e-08;

Matches 25; Conservative 19; Mismatches 31; Indels 1; Gaps 1;

Db 12 TENNDHNLKVAGQDCS-VVQFKIKRHTPISKLMKAYCERQGLSMRQIRPFRDGQPINE 70

RT "SMT3A, a human homologue of the *S. cerevisiae* SMT3 gene, maps to chromosome 21qter and defines a novel gene family.";

RL GENOMICS 40:362-367(1997);

CC -!- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.

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CC DR EMBL; X99609; E229962; -;

CC DR PROSITE; PSS0053; UBIQUITIN\_2; 1.

CC FT DOMAIN 16 93 UBIQUITIN-LIKE.

CC SQ SEQUENCE 104 AA; 11654 MW; CD7D6439 CRC32;

Query Match 5.6%; Score 160; DB 1; Length 104; Best Local Similarity 25.7%; Pred. No. 1.4e-07; Matches 19; Conservative 26; Mismatches 28; Indels 1; Gaps 1;

Db 13 DSGGAHINLKVKQDGNEVF-FRIKRSQQLKLMNAYCDROSVDMNNSIAFLFDGRRLRRAEQ 71

CC QY 336 EFGQELRIVQKEKKHOMLEISLSPDSLPLKVLMSHYEAMGLSGHKLSFFFDTKISGKE 395

Db 72 TDEDELMDGEDEID 85

CC QY 396 LPADLGESGLIE 409

DR UBIQUITIN-LIKE PROTEIN SMT3.

GN SMT3.

OS CAENORHABDITIS ELEGANS.

OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RN [1] SEQUENCE FROM N.A.

RX MEDLINE: 97237059

RA LAPENTA V., CHIURAZZI P., VAN DER SPEK P.J., PIZZUTI A., BRAHE C., HANOKA F.,

RT "SMT3A, a human homologue of the *S. cerevisiae* SMT3 gene, maps to chromosome 21qter and defines a novel gene family.";

RT GENOMICS 40:362-367(1997).

RN [2] SEQUENCE FROM N.A.

RX MEDLINE: 97318858

RA CHODHURY B.K., LI S.S.,

RT "Identification and characterization of the SMT3 cDNA and gene from nematode *Caenorhabditis elegans*";

RL BIOCHEM. BIOPHYS. RES. COMMUN. 234:788-791(1997);

CC -!- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.

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CC DR EMBL; X99600; E259960; -;

CC DR EMBL; U94830; G2241095; -;

CC DR PROSITE; PSS0053; UBIQUITIN\_2; 1.

CC FT DOMAIN 13 91 UBIQUITIN-LIKE.

CC SQ SEQUENCE 91 AA; 10222 MW; F8E538FD CRC32;

RESULT 3

ID SMT3\_ARATH STANDARD; PRT; 104 AA.

AC P55852;

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE UBIQUITIN-LIKE PROTEIN SMT3.

GN SMT3.

OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

OC EUPHYLLIOPHTHE; SPERMATOPHTHA; MAGNOLIOPHTHA; OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.

OC [1] SEQUENCE FROM N.A.

RX MEDLINE: 97237059

RA LAPENTA V., CHIURAZZI P., VAN DER SPEK P.J., PIZZUTI A., BRAHE C., HANOKA F., BRAHE C.,

Query Match	5.3%	Score 152; DB 1; Length 91;
Best Local Similarity	22.3%	Pred. No. 1. 1.55e-06;
Matches	18;	Conservative 31; Mismatches 30; Indels 1; Gaps 1;
ID	SM33_HUMAN	STANDARD; PRT; 101 AA.
AC	P55856;	093058; P55856.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-DEC-1998	(REL. 37, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1)	
GG	(GAP MODIFYING PROTEIN 1) (GMPI) (SENTRIN).	
SM	SMT3H OR SMT3C.	
DN	HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN; TISSUE=BRAIN;	
EC	MEDLINE: 97231059.	
CC	LAPERNA V., CHIURAZZI P., VAN DER SPEK P.J., PIZZUTI A.,	
CA	HANAKA F., BRAKE C.;	
BT	"SMT3A, a human homologue of the <i>S. cerevisiae</i> Smf3 gene, maps to chromosome 21qter and defines a novel gene family.";	
GT	GENOMICS 40:3362-3367(1997).	
GN	[2]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
EC	MEDLINE: 9640311.	
CA	BODDY M.N., HONE K., ETKIN L.D., SOLOMON E., FREEMONT P.S.;	
BT	"PIC 1, a novel ubiquitin-like protein which interacts with the PML component of a multi-protein complex that is disrupted in acute promyelocytic leukaemia";	
GT	ONCOGENE 13:971-982(1996).	
GN	[3]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN;	
EC	MEDLINE: 9641684.	
CA	CHEN D.J.; PARDINGTON-PURTYMUN P.E., COMEAUX J.C., MOYZIS R.K.,	
BT	"UBL1, a human ubiquitin-like protein associating with human RAD51/RAD52 proteins";	
GT	GENOMICS 36:271-279(1996).	
GN	[4]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN;	
EC	MEDLINE: 97146692.	
CA	MAHAJAN R., DELPHIN C., GUAN T., GERACE L., MELCHIOR F.;	
BT	"A small ubiquitin-related polypeptide involved in targeting RanGAP1 to nuclear pore complex protein RanBP2.;"	
GT	CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	5	Score 152; DB 1; Length 91;
ID	SM31_HUMAN	STANDARD; PRT; 101 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=MOUSE; STRAIN=ICR;	
EC	MEDLINE: 9812640.	
CA	HOWE K., WILLIAMSON J., BODDY M.N., SHEER D., FREEMONT P.S.,	
BT	SOLOMON E.;	
GT	"The ubiquitin-homology gene PIC1: characterization of mouse (Pic1) and human (Ubl1) genes and pseudogenes.;"	
GN	GENOMICS 47:92-100(1998).	
LP	[8]	
CC	STRUCTURE BY NMR.	
CA	RAY BAYER P., ARNDT A., METZGER S., MAHARAN R., MELCHIOR F., JAENICKE R., BECKER J.;	
BT	"Structure determination of the small ubiquitin-related modifier SUMO-1.";	
GT	MEDLINE: 98319859.	
GN	J. MOI. BIOL. 280:275-286(1998).	
LP	[1]	
CC	FUNCTION: ASSOCIATES WITH RAD51/RADS2. INVOLVED IN TARGETING RANGAP1 TO THE NUCLEAR POLE COMPLEX PROTEIN RANBP2.	
CC	-1 SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstations on the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@lsb-sib.ch).	
CC	[2]	
DR	EMBL; X99586; E274603; -.	
DR	EMBL; U61391; G151894; -.	
DR	EMBL; U30784; G157948; -.	
DR	EMBL; U61122; G176297; -.	
DR	EMBL; U72722; G170503; -.	
DR	EMBL; U83117; G1769602; -.	
DR	EMBL; AF033353; G2645737; -.	
DR	MIM: 601912; -.	
DR	PDB; 1A5R; 14-OCT-98.	
DR	PDB; 1A5P; PS50053; UBIQUITIN_2; 1.	
KW	PROSITE; PROSITE; PS50053; UBIQUITIN_2; 1.	
FT	3D-STRUCTURE.	
FT	DOMAIN 20: 101 AA; 1155 MW; EC25CIFE CRC32; SEQUENCE 101 AA; 1155 MW; EC25CIFE CRC32;	
Query Match	5.2%	Score 149; DB 1; Length 101;
Best Local Similarity	28.6%	Pred. No. 4. 0.07e-06;
Matches	20;	Conservative 23; Mismatches 26; Indels 1; Gaps 1;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	
SP	SEQUENCE FROM N. A.	
PC	SPECIES=HUMAN;	
EC	MEDLINE: 97133418.	
CA	MATUNIS M.J., COUTAVAS E., BIEBEL G.;	
BT	"A novel ubiquitin-like modification modulates the partitioning of the Ran-GTPase-activating protein RanGAP1 between the cytosol and the nuclear pore complex.;"	
GT	J. CELL BIOL. 135:1457-1470(1996).	
GN	[6]	
LP	SEQUENCE FROM N. A.	
CC	SPECIES=HUMAN; TISSUE=PLACENTA;	
RESULT	6	Score 149; DB 1; Length 101;
ID	SM31_HUMAN	STANDARD; PRT; 103 AA.
AC	P55854;	055854; P55854.
DT	01-NOV-1997	(REL. 35, CREATED)
BT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)
LT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)
PI	UBIQUITIN-LIKE PROTEIN SMT3A.	
GG	SMT3H OR SMT3A.	
DN	HOMO SAPIENS (HUMAN);	
SC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
PR	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	
CC	[1]	

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
 RN [1] CC  
 RP CC  
 RC CC  
 RX TISSUE-BRAIN;  
 MEDLINE; 97237059.  
 RA LAPENTA V., CHIARAZZI P., VAN DER SPEK P.J., PIZZUTI A.,  
 RA HANAKA F., BRAHE C.;  
 RT "SMT3A", a human homologue of the *S. cerevisiae* SMT3 gene, maps to  
 RT chromosome 21qter and defines a novel gene family.;  
 RL GENOMICS 40:362-367(1997).  
 CC  
 CC -1- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.  
 CC  
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 CC  
 DR EMBL; L22090; GA04775; --.  
 DR PROSITE; PS00030; RNP\_1; FALSE NEG.  
 DR INITIATION FACTOR; PROTEIN BIOSYNTHESIS; PHOSPHORYLATION;  
 KW RNA-BINDING.  
 FT DOMAIN 188 192 POLY-PRO.  
 FT DOMAIN 262 275 POLY-GLU.  
 FT DOMAIN 602 607 RNA-BINDING (RNP2) (BY SIMILARITY).  
 FT DOMAIN 698 706 RNA-BINDING (RNP1) (BY SIMILARITY).  
 SQ DOMAIN 1393 1399 POLY-GLU.  
 SQ SEQUENCE 1402 AA; 1540550 MW; 6B00C346 CRC32;  
 Query Match 4.9% Score 141; DB 1; Length 103;  
 Best Local Similarity 30.4%; Pred. No. 5.1e-05;  
 Matches 24; Conservative 20; Mismatches 33; Indels 2; Gaps 2;  
 Db 8 EGYKTENDHNIRKVAGODGS-VVQPKLKRHTLSKLMAKAYCERQGIGSMQRQIRFRFDQOPTI 66  
 Qy 333 EATETSQE-LRURVGKREKHOMLEISLSPDSPLVKVLMSHYEAMGLSGHKLSSFFDSTKL 391  
 Db 67 NEFTDPQLRMDEDDTIDY 85  
 Qy 392 SGKELPADLGLESSGDLLIEV 410  
 RESULT 7 ID4G-RABBIT STANDARD; PRT; 1402 AA.  
 AC P4110;  
 AC P4110;  
 DT 01-FEB-1995 (REL. 31, CREATED)  
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DT EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (EIF-4-GAMMA) (EIF-4G)  
 (EIF4G) (P220).  
 OS ORCTOLAGUS CUNICULUS (RABBIT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC LAGOMORPHA; LEPODIA; ORCTOLAGUS.  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 479-500.  
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=BRAIN;  
 RX MEDLINE; 93374895.  
 RA LAMPHEAR B.J., YAN R., YANG F., WATERS D., LIEBIG H.-D.,  
 RA KLUMP H., KUECHLER E., SKERN T., RHODES R.E.;  
 RT Mapping the cleavage site in protein synthesis initiation factor  
 RT eIF-4 gamma of the 2A proteases from human Coxsackievirus and  
 RT rhinovirus.;  
 RL BIOL. CHEM. 268:19200-19203(1993).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RX MEDLINE; 93054654.  
 RA VAN R., RYCHLIK W., EICHISON D., RHODES R.E.;  
 RT "amino acid sequence of the human protein synthesis initiation factor  
 RT eIF-4 gamma.";  
 RL J. BIOL. CHEM. 267:23226-23231(1992).  
 CC -1- FUNCTION: COMPONENT OF THE PROTEIN COMPLEX EIF-4, WHICH IS  
 INVOLVED IN THE RECOGNITION OF THE mRNA CAP, ATP-DEPENDENT  
 CC UNWINDING OF 5'-TERMINAL SECONDARY STRUCTURE AND RECRUITMENT OF  
 CC mRNA TO THE RIBOSOME.  
 CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).  
 DR PROSITE; PS00053; UBIQUITIN\_2; 1.  
 DR EMBL; X99584; E274634; --.  
 DR MMDB; 602331; --.  
 DR PROSITE; PS00053; UBIQUITIN\_2; 1.  
 DR DOMAIN 15 92 UBIQUITIN-LIKE.  
 DR SEQUENCE 103 AA; 1654 MW; 6B303BC0 CRC32;  
 Query Match 4.9% Score 141; DB 1; Length 103;  
 Best Local Similarity 30.4%; Pred. No. 5.1e-05;  
 Matches 24; Conservative 20; Mismatches 33; Indels 2; Gaps 2;  
 Db 482 ALSSRG-P-PRGGPGGLPGRGAAGLGLQRLPPKGKRLASIVMTEDIKLNAAEKAW 540  
 Qy 4 PLRGPRGRSRGGRGARRGARGRCRGRQSPARLIPDVTWLVSDSEEVLEYADPVE 63  
 Db 541 KPSKSKRAADD-DR-GBEDADGSKTODLFRKVRSILNLTKPQMFOQLMKVQTLAIDTEG 598  
 Qy 64 WPVVARLPAPAKPEQDSDSDSGA-AEGPAGAPRILVRRRRRLDPGEAPVVPV-YSGKV 121  
 Db 599 ASKGSLTSLLRPFPQNTSPSPSQRHYPPLPHGAEATKEPKPTVN-FRKILLNRQKEFE 657  
 Qy 122 QSSLNLDIPDNSSLKLCPSE-PEADEALTNQGSSPSEDDAL-PSGSPWRKKLRKKE-E 179  
 Db 658 KDKDDEVFEKKKEMEAAEERLKEELEARDIAR 698  
 Qy 180 K-KME-EFPDDDISPLQPSPRSRNRSKXTEALQKUREVR 218  
 RESULT 8 ID SMT3-SCHPO STANDARD; PRT; 90 AA.  
 AC O13351;  
 DT 15-JUL-1998 (REL. 36, CREATED)  
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
 DE UBIQUITIN-LIKE PROTEIN SMT3.  
 GN SMT3.  
 OS SCHIZOSACCHAROMYCETES POMBE (FISSION YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;  
 OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;  
 OC SCHIZOSACCHAROMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=358;  
 RA PELLETIER M.F., DIGNARD D.;  
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDJB DATA BANKS.  
 CC -1- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.  
 CC  
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 CC  
 DR EMBL; AF019235; G244268; --.  
 DR PROSITE; PS00053; UBIQUITIN\_2; 1.  
 DR DOMAIN 7 87 UBIQUITIN-LIKE.

**SQ** SEQUENCE 90 AA; 10240 MW; F2CAD69A CRC32;  
 Query Match 4.4%; Score 126; DB 1; Length 90;  
 Best Local Similarity 27.4%; Pred. No. 4.80e-03; Mismatches 30; Indels 1; Gaps 1;  
 Matches 20; Conservative 22; Mismatches 30; Indels 1; Gaps 1;  
  
**Db** 5 STEPHINKVVGDDNNEVF-FKIKKTFPSKLMMKTCARQGKSMNSLRLFLVGERIRRPDQT 63  
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
**Oy** 337 TSQLRLRVQSKKEKHOMLEISLSPDPLKVLMHYEARMLGKLSFFDGTKLKGKEL 396  
  
**Db** 64 PAFEDMEGGDIE 76  
 |||:|||||||  
**Oy** 397 PADLGLESGLIE 409

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**RESULT** 9 STMT 3 YEAST STANDARD; PRT; 101 AA.  
**ID** SMT3 YEAST  
**AC** 012305; 01-NOV-1997 (REL. 35, CREATED)  
**DT** 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
  
**GN** UBIQUITIN-LIKE PROTEIN SM3  
 SMT3 OR YD2510W OR D9719.15.  
  
**OS** SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)  
**OC** EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;  
**RC** [1] SACCHAROMYCETACEA; SACCHAROMYCES.  
  
**RP** SEQUENCE FROM N.A.  
  
**RA** STRAIN=YPHLYNN14;  
  
**RA** MELUH, P.B.; KOSHLAND, D.E.;  
**RL** SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.  
**RN** [2]

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**PP** SEQUENCE FROM N.A.  
  
**RA** DIETRICH, F.S.;  
  
**RL** SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.  
  
**CC** --!- FUNCTION: NOT KNOWN; SUPPRESSOR OF MTF2 MUTATIONS.  
**CC** --!- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SM3 SUBFAMILY.

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**CC**  
  
**DR** EMBL; U27233; G881372; -.  
**DR** SGD; L0001938; SMT3.  
**DR** PROSITE; PS50053; UBIQUITIN-2; 1.  
**DT** DOMAIN 22; 101 AA; UBIQUITIN-LIKE.  
**GT** SEQUENCE 101 AA; 11597 MW; A2C509ED CRC32;

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**RESULT** 11 ID BAT2\_HUMAN STANDARD; PRT; 2142 AA.  
**ID** BAT2\_HUMAN  
**AC** P48634;  
**DT** 01-FEB-1996 (REL. 33, CREATED)  
**DT** 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
**DT** 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
**DE** LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).  
**GN** BAT2.  
  
**OS** HOMO SAPIENS (HUMAN)  
**OC** EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
**OC** PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
**RN** [1] SEQUENCE FROM N.A.  
  
**RP** TISSUE-T-CELL;  
  
**RX** MEDLINE; 90192810.  
  
**RA** BANERJI, J., SANDS, J., STROMINGER, J.L., SPIES, T.  
**RT** "A gene pair from the human major histocompatibility complex encodes large proline-rich proteins with multiple repeated motifs and a single ubiquitin-like domain." PROC. NATL. ACAD. SCI. U.S.A. 87:2374-2378(1990).  
  
**RN** [2] SEQUENCE OF 1-1860 FROM N.A.  
**RX** MEDLINE; 93272029.  
**RA** IRIS, F.J.M., BOUGUERET, L., PRIEUR, S., CATERINA, D., PRIMAS, G.,  
**DE** FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 2.  
**RA** PERRI, V., JURKA, J., RODRIGUEZ-TOME, P., CLAVIERE, J.-M., DAUSSET, J.,  
**RA** COHEN, D.  
**RT** "Dense Ali cluster and a potential new member of the NF kappa B family within a 90 kilobase HLA class III segment." PRO





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CC or send an email to licensee@sb-sib.ch).

DR	EMBL; X69955; G1961;	-.
DR	PIR; S11034; S11034.	
DR	FYBRE; F1gn000639; Fbp1.	
DR	PFAM; PF00372; hemocyanin;	2.
KW	SIGNAL; GLYCOPROTEIN.	
FT	SIGNAL	16
FT	CHAIN	17
FT	DOMAIN	360
FT	DOMAIN	580
FT	CARBOND	741
SO	SEQUENCE	1030 AA;
		119365 MW;
		A3AC5F31 CRC32;
		POTENTIAL. FAT-BODY PROTEIN-1.
		POLY-ASP.
		POLY-ASP.
		POTENTIAL.

Query Match 3.9%; Score 111; DB 1; Length 1030;  
 Best Local Similarity 20.9%; Pred. No. 3. 3.3e-01;  
 Matches 42; Conservative 66; Mismatches 76; Indels 17; Gaps 15;

Db 559 TDDTELEMQRNROORLQKH-QNDQQD-DD-NDDDVVNVHROGLASRSRLPNLROQNNRL 615  
::| :| ::| :| ::| :| ::| :| ::| :| ::| :| ::| :| ::| :| ::| :| ::| :| ::| :|  
QY 156 SEDDAFLPS-GSPWKRKKLCKEEKMMETFPDDQDISPLPOPSSRNKSRKHTEAQLRLE 214  
Db 616 SEIVLHMLRQ-LVARINGQEESTAQOQJEEQDQLINPRQSERIALRLOMIRINSORSR 674

QY	215	VNRKLDLRSCLSPKHOHSPALQS--TDDEVLVLEGPVLPOSSRL-FTLIL-IRCRADLVR	270
Db	675	OVALQIGOIEQRIOEVIGOVLSQVNNTSLRQEVIDORQVSILIAVLGLGQVGIMTII	734

QY  
271 --Lp--v--RMSEPLQNVWDHMANHLGG  
Db 735 RQWQDNNSEQIDRNGLGIRL 755  
Qy 324 DCVVLASSATE-TSQELRL 343

Search completed: Fri Feb 18 11:59:27 2000  
Job time : 51 secs.

Job time : 51 secs.







OS HOMO SAPIENS (HUMAN). CHORDATA; MAMMALIA; EUTHERIA; PRIMATES;  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC CATHARRHINI; HOMINIDAE; HOMO.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SELELPT MUSCLE;  
 RA OSBORNE L.R., JADAVEL D.M., COIGNET L.J., ZANI V.J., TSUI L.C.,  
 RA SCHERER S.W., DYER M.J.;  
 RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDJB DATA BANKS.  
 DR EMBL: A1223980; E124984; -.  
 SQ SEQUENCE 217 AA; 23365 MW; D15BB4BE CRC32;

Query Match 4.1%; Score 118; DB 4; Length 217;  
 Best Local Similarity 26.1%; Pred. No. 1.25e-01; Indels 12; Gaps 11;  
 Matches 40; Conservative 41; Mismatches 60; RT STRAIN=H37RV;  
 RC STRAIN=H37RV;  
 RA COLE S.T., BARRELL B.G., RAJANDREAM M.A.;  
 RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDJB DATA BANKS.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE; 96181548.  
 RA PHILIP W.J., POULET S., REIGLMEIER K., PASCOPILLA L.,  
 RA BALASUBRAMANIAN V., HYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,  
 RA COLE S.T.;  
 DT 114 SPGGTOPSPSRPVSAGPPEGVPEEAQPPRIGQEDPGGGTAGSTDDEPMLTKEPVPPELL 173  
 DR :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 QY 71 APA-KPEQDSDSSEGAAEG-PAGA-PRTLVRRRRRLDPGPAPVPPVVIS GK-VSSL 125  
 Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium  
 leprae.;  
 PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).  
 DR EMBL: 295436; E316541; -.  
 DR PFAM: PF00271; helicase\_C; 1.  
 KW HYPOTHEICAL PROTEIN.  
 SQ SEQUENCE 771 AA; 81409 MW; 48B7AFB6 CRC32;

RESULT 11  
 ID 07-038 PRELIMINARY; PRT; 425 AA.  
 AC 075038;  
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)  
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)  
 DE KIAA0450 PROTEIN.  
 GN KIAA0450.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
 OC CATHARRHINI; HOMINIDAE; HOMO.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE; 98116662.  
 RA NOMURA N., OHARA O.;  
 RA ISHIKAWA K., MIYAJIMA N., NAKAJIMA D.,  
 RA SEKI N., OHIRA M., NAGASE T., ISHIKAWA K., MIYAJIMA N., NAKAJIMA D.,  
 RA "Characterization of cDNA clones in size-fractionated cDNA libraries  
 from human brain,"  
 RL DNA RES. 4:315-349(1997).  
 DR EMBL: A8007919; D1033257; -.  
 SQ SEQUENCE 425 AA; 43842 MW; 0064808E CRC32;

Query Match 4.1%; Score 117; DB 4; Length 425;  
 Best Local Similarity 31.5%; Pred. No. 1.63e-01; Indels 25; Mismatches 43; Gaps 8; RT STRAIN=H37RV;  
 RC DNA RES. 4:315-349(1997).  
 RL EMBL: A8007919; D1033257; -.  
 SQ SEQUENCE 425 AA; 43842 MW; 0064808E CRC32;

RESULT 13  
 ID 065511 PRELIMINARY; PRT; 210 AA.  
 AC 065511;  
 DT 01-NOV-1995 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DE HERPESVIRUS-7 (HHV7) JI, COMPLETE VIRION GENOME (FRAGMENT).  
 GN U80.  
 OS HUMAN HERPESVIRUS TYPE 7.  
 OC VIRUSES; DSNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;  
 OC BETAHERPESVIRINA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JI;  
 RA NICHOLAS J.;  
 RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDJB DATA BANKS.  
 DR EMBL: U43400; G1139682; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 210 AA; 23935 MW; EC2EE0D9 CRC32;

Query Match 4.0%; Score 114; DB 14; Length 210;  
 Best Local Similarity 46.9%; Pred. No. 3.61e-01; Indels 3; Mismatches 23; Gaps 3; RT STRAIN=H37RV;  
 RC STRAIN=H37RV;  
 RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDJB DATA BANKS.  
 DR 149 STRSRGSRGRGRC-RSRNMSMRQTP-REVEMDPIVILSDPSRETL 195  
 QY 9 GPRRSRG-QGRGARRGARGCPRAROSPARLIPDPDVLDVLSDSDEEV 56  
 DE HYPOTHETICAL 81.4 KD PROTEIN.  
 GN MTCY15C10.03C.

RESULT 14 KW HYPOTHETICAL PROTEIN.  
 ID 020393 PRELIMINARY; SQ SEQUENCE 506 AA; 58462 MW; 957FD02B CRC32;  
 AC 020393: PRT; 352 AA.  
 DT 01-NOV-1995 (TREMBREL. 01, CREATED)  
 DT 01-NOV-1995 (TREMBREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1999 (TREMBREL. 09, LAST ANNOTATION UPDATE)  
 DE F44D12.4 PROTEIN.  
 GN F44D12.4.  
 OS CAENORHABDTIS ELEGANS.  
 OC EUKARYOT; METZOA; NEMATODA; SECERNENTIA; RHABDITIA; RHABDITID; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINA; CAENORHABDTIS.  
 OC [1]  
 RN SEQUENCE FROM N.A.  
 RA COLES L.;  
 RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDJB DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94150718.

[2]

SEQUENCE FROM N.A.

RP

MEDLINE:

94150718.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,

BONFIELD J., BURTON J., CONNELL M., COSEY T., COOPER J., COULSON A.,

CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

GARDNER A., GREEN P., HAWKINS T., HILLER L., JIEER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., McMURRAY A., MORTMORE B., O'CALLAGHAN M.,

PARSONS J., PERCI C., RIFKEN L., ROOPRA A., SAUNDERS D., SHAWNKEEN R.,

SMALDON N., SMITH A., SONNHAMMER E., SPADEN R., SULSTROM J.,

THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSON R.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P.,

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans".

RT NATURE 368:32-38(1994).

RL

EMBL: Z60298; E134770; -.

DR

SEQUENCE

352 AA;

39367 MW;

2EA853D3 CRC32;

SQ

SEQUENCE

506 AA;

58462 MW;

957FD02B CRC32;

Query Match 4.0%; Score 114; DB 14; Length 506;  
 Best Local Similarity 46.9%; Pred. No. 3.61e-01; Mismatches 15; Indels 3; Gaps 3;  
 Matches 23; Conservative 8; Mismatches 15; Indels 3; Gaps 3;  
 Db 445 STRSRGRSRGRPRORG-RSRNMSRQTP-REVEMLPTVLDSDSDTETL 491  
 Qy 9 GPRSGR-GGRARRARGRGRCPRARQSPARLIPDVLDVSDSDEEVL 56

Search completed: Fri Feb 18 12:01:45 2000

Job time : 120 secs.

Query Match 4.0%; Score 113; DB 5; Length 352;  
 Best Local Similarity 29.2%; Pred. No. 4.69e-01; Mismatches 19; Indels 2; Gaps 1;  
 Matches 19; Conservative 19; Mismatches 25; Indels 2; Gaps 1;

Db 1 M0SGAPCRRSSRSRSGAFNR-RSNYGEAHITQPAVLASTVEPSSIMPVYNPLAV 58  
 Qy 5 LRGIGPRSRGRRGARRGARGRCPRAROSPARLIPDVLDVSDSDEEVLEVADPVEV 64

Db 59 AAEL 63  
 Qy 65 PVARL 69

RESULT 15 KW HYPOTHETICAL PROTEIN.  
 ID 056296 PRELIMINARY; SQ SEQUENCE 506 AA;  
 AC 056296; PRT; 506 AA.  
 DT 01-JUN-1998 (TREMBREL. 06, CREATED)  
 DT 01-NOV-1998 (TREMBREL. 08, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 58.5 KD PROTEIN.  
 GN U79.  
 OS HUMAN HERPESVIRUS 7.  
 OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;  
 OC BETAHERPESVIRINAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RK;  
 RX MEDLINE: 9824091.  
 RA MEGAW A.G., RAPAPORT D., AVIVOR B., FRENKEL N., DAVISON A.J.,  
 RT "The DNA sequence of the RK strain of human herpesvirus 7.",  
 RL VIROLOGY 244:119-132(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RK;  
 RA MEGAW A.G., FRENKEL N., DAVISON A.J.;  
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDJB DATA BANKS.  
 EMBL: AF037218; G2746308; -.

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